Structure

In This Issue

Import Receptors of Peroxisomes, Mitochondria, and Plastids under One Roof

PAGE 1783

Specific targeting of proteins to unique cellular compartments is an essential feature of eukaryotic cells. Understanding this specificity at a molecular level requires a structural insight into the specific receptors involved. Panigrahi et al. review the molecular details underlying various import receptors from the outer membranes of peroxisomes, mitochondria, and plastids.

Bromodomains Meet Butyryllysines and Crotonyllysines

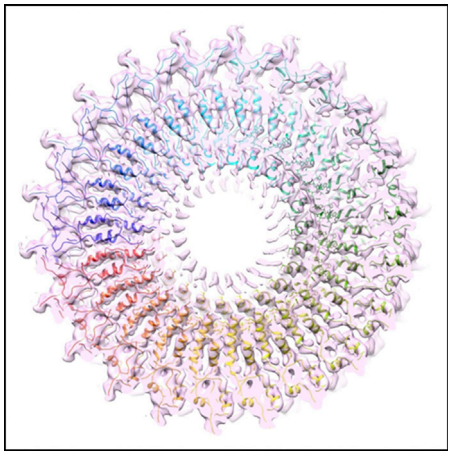
PAGE 1801

Bromodomains are protein modules that "read" acetyllysine marks on histone tails. Flynn et al. screen human bromodomains for binding to less common histone acyl modifications and find candidate bromodomain readers for butyryl- and crotonyllysine. Crystal structures reveal how these unusual modifications are accommodated.

How Barley Stripe Mosaic Virus is Held Together

PAGE 1815

Clare et al. determine the structure of barley stripe mosaic virus at 4.1 Å and find that there are 2 distinct virions. The authors find a new lateral contact between the capsid proteins that is essential for viron stability.



Global Genome Repair through an XPC Lens

PAGE 1827

In global genome repair (GGR), XPC detects damaged nucleotides and recruits TFIIH complex. Okuda et al. present the tertiary structure of XPC bound to the pleckstrin homology domain of TFIIH subunit p62 by NMR, reveal the recognition mechanism, and show the significance of the interaction for GGR.

Mapping the Origin of the Molecular Switch Proteins

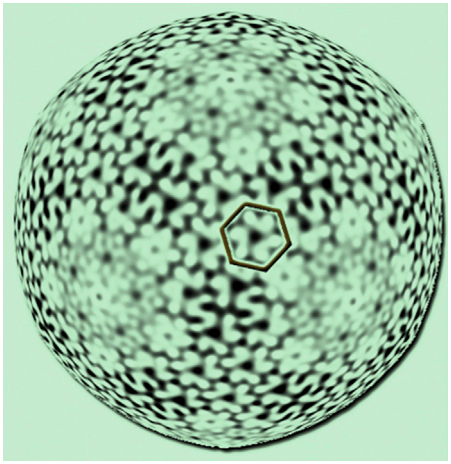
PAGE 1838

Small molecular switch proteins are tracers for eukaryotic evolution. The earliest branching involves three GTPases associated with cellular membranes. Jadhav et al. present structures and switch cycle of the SRβ subunit of the signal recognition particle receptor that targets nascent protein chains to the endoplasmic reticulum.

An Interaction Hub in Autophagy

PAGE 1848

The human ULK1-FIP200-Atg13-Atg101 complex initiates autophagy and is a promising target for aging, neurodegeneration, cancer, and infection. Qi et al. describe a structure of the HORMA dimer of human Atg13 and Atg101 that shows how they assemble and might coordinate binding of substrates and regulatory proteins.



Ribosomal Silencing Factor Puts a Stop to a Ribosome

PAGE 1858

Li et al. report the crystal structure of *Mycobacterium tuberculosis* (*Mtb*) ribosomal silencing factor RsfS and the cryo-electron microscopy structure of *Mtb* ribosome large subunit 50S complexed with RsfS, which reveals the inhibition of protein synthesis by RsfS via blocking the association of ribosome 30S.

Vertical Single β-Barrel Capsid Proteins and a Pinch of Salt

PAGE 1866

Gil-Carton et al. present biochemical and structural studies of archaeal, halophilic HHIV-2 virus. The cryo-electron microscopy based structure shows how membrane-protein interactions below the capsid could serve as protein-railing for guiding the assembly of the two vertical single β-barrel major capsid proteins. Disulfide bonds cement the virus structure.

BAX Oligomerization Precedes Membrane Insertion

PAGE 1878

Sung et al. use ESR to reveal a complete solution structure of apoptotic BAX protein oligomer. The results suggest an alternative pathway of apoptosis in which BAX oligomer formation occurs prior to membrane insertion.

Mammalian Peptide Transport Becoming Crystal Clear

PAGE 1889

The crystal structure of PepT1 and PepT2 reported by Beale et al. reveals two immunoglobulin-like domains connected in tandem inserted within the canonical major facilitator superfamily fold. Biophysical analyses reveal a specific interaction with trypsin, suggesting a role in clustering proteolytic activity to the site of peptide uptake across membrane.

Going Green

PAGE 1900

Han et al. determine a structure of Xanthomonas type III effector AvrRxo1-ORF1:ORF2. The AvrRxo1-ORF1:ORF2 complex is structurally homologous to zeta toxin:epsilon antitoxin. Expression of AvrRxo1-ORF1 suppresses bacterial growth depending on its kinase motif. AvrRox1-ORF1 has significant virulence function that can increase bacterial growth on the host plant.

Coupled Folding and Binding in Endosomal Cargo Trafficking

PAGE 1910

Tollip and Tom1 are adaptor proteins that participate in endosomal cargo trafficking. Xiao et al. establish that Tollip TBD undergoes a Tom1 GAT-mediated folding-upon-binding mechanism that is required to inhibit binding of Tollip to phosphatidylinositol 3-phosphate.

MLL Family SET Domain that Keeps Going

PAGE 1921

The MLL family of histone H3K4-specific methyltransferases contains six members, each with a unique role. Zhang et al. show that, unlike MLL1, the MLL4 SET domain has high intrinsic activity without the cognate complex. The authors have identified a new structural element that contributes to this intrinsic activation.

Structural Basis of Telomerase Inhibition

PAGE 1934

BIBR1532 is a highly selective inhibitor of telomerase that has a direct antiproliferative effect on leukemia cells. Bryan et al. provide an atomic view of telomerase in complex with a small molecule inhibitor and stands to reinvigorate the field of telomerase inhibition using a structural biology approach.

Natively Glycosylated HIV-1 Env Protein

PAGE 1943

Env is the heavily glycosylated fusion machinery of HIV-1. Using cryoEM, Lee et al. present an atomic model of broadly neutralizing antibody PGT128 in complex with a fully glycosylated Env that reveals the native, intact epitope.

PTEN Homodimerization

PAGE 1952

Heinrich et al. show that the phosphatase domains of PTEN form a homodimer that is likely stabilized through a domain-swapping interaction of the two C-terminal tails. This provides a structural basis for the PTEN dimer hypothesis and sheds new light on cellular control via tail phosphorylation.

Follow the COMPASS

PAGE 1958

Courtney et al. develop an algorithm that scores protein structural models against a previously unanalyzed NMR spectrum. This method, named COMPASS, does not require chemical shift assignments and identifies the correct structure in most cases within 1.5 Å RMSD of the reference structure.

